

**IN THE CLAIMS:**

Please amend claims 11 and 16 as follows:

1. (Previously Amended) An isolated rpoB nucleic acid molecule consisting of at least about 100 contiguous bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9 and 10.
2. (Previously Amended) An isolated nucleic acid molecule consisting of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9 and 10.
3. (Previously Amended) A probe which is the complement of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.
4. (Previously Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;  
determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;  
comparing the determined sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and  
classifying the mycobacteria from the extent of similarity of the compared sequences.
5. (Original) The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.
6. (Previously Amended) The method of claim 4, wherein the determined sequence is compared with at least nine sequences selected from the group consisting SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.
7. (Previously Amended) A method of classifying a mycobacteria, comprising

providing a sample comprising a mycobacterial *rpoB* target nucleic acid;  
determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more bases in a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10, wherein the one or more bases of the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 differ from the corresponding one or more bases in SEQ ID NO. 1 when the sequences are maximally aligned, the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample;

comparing the identified one or more bases in the target sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and

classifying the mycobacteria from the extent of similarity between the one or more bases identified in the target sequence and the corresponding one or more bases in the compared sequences.

8. (Previously Amended) The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

9. (Previously Amended) The method of claim 8, wherein the identity of at least 20 bases in the target sequence at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

10. (Previously Amended) The method of claim 9, further comprising comparing the at least 20 determined bases with at least 20 bases occupying corresponding positions in each of at least nine sequences selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

11. (Presently Amended) A polynucleotide probe or primer that hybridizes under stringent hybridization conditions to ~~[at least a contiguous segment of]~~ a mycobacterial *rpoB* sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 or its

complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO: 1 or its complement, ~~[wherein the contiguous segment of the mycobacterial rpoB sequence includes at least about 5 bases of the mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding at least about 5 bases in SEQ ID NO: 1 when the sequences are maximally aligned;]~~ wherein said stringent hybridization conditions comprise 5 x SSPE and a temperature of 25-30°C.

12. (Previously Amended) The polynucleotide of claim 11 that is a probe.

13. (Currently Amended) The polynucleotide of claim 12, wherein a central position of the probe aligns with ~~[the]~~ one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

14. (Previously Amended) The sequence-specific polynucleotide of claim 11 that is a primer.

15. (Currently Amended) The polynucleotide of claim 14, wherein the 3' end of the primer aligns with ~~[the]~~ one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

16. (Currently Amended) The polynucleotide of claim 11 that hybridizes under stringent hybridization conditions to at least 100 contiguous bases of a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 or its **complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO:1 or its complement.**

***REMARKS***

The Office Action mailed March 25, 2003 and the Advisory Action mailed July 3, 2003 have been carefully reviewed and the foregoing amendments are made in response thereto. In view of the amendments and the following remarks, Applicants respectfully request reconsideration and reexamination of this application and the timely allowance of the pending claims.

Applicants respectfully submit that no prohibited new matter has been introduced by the amendments. Support for the amendments to the claims can be found throughout the specification and claims as originally filed. The amendment to claim 16 is made to correct an inadvertent truncation in claim 16 as it appeared at page 4 of the Amendment and Response filed January 6, 2003. Entry of the amendment is respectfully requested.

***Advisory Action***

The Advisory Action mailed July 3, 2003 indicates the following with respect to the Amendment After Final filed June 19, 2003:

The amendment to claim 1, if entered, would overcome the rejections under 35 U.S.C. § 112, first paragraph (written description) and 35 U.S.C. § 112, second paragraph.

The amendment to claim 11, if entered, would not overcome the rejection under 35 U.S.C. § 102(b) because it is alleged that the term “fully complementary” refers to a contiguous portion and not necessarily the whole SEQ ID NO.

The arguments with respect to the rejection of claims 11-16 under 35 U.S.C. § 112, first paragraph (written description) are not persuasive because a specific designation of a lower limit of at least five was not found.

***Status of the Claims***

Claims 1-16 are pending. The Amendment filed January 6, 2003 has been entered, the Amendment After Final, filed June 19, 2003 was not entered.

***Specification***

Applicants acknowledge, with appreciation, the indication made on the Office Action Summary (Paper No. 33) mailed March 25, 2003 that the formal drawings filed on April 4, 2002

have been accepted. Applicants also note that the claim for domestic priority under 35 U.S.C. § 119(e) has been acknowledged by the Office.

The Office Action, at page 2 objects to the specification because it is alleged that the phrase <http://www.ncbi.nlm.nih.gov/> appearing on page 8, line 18 would be recognized as a live web link if it were to appear as text on the USPTO web site in the form of a patent. Without acquiescing to the grounds of the rejection, Applicants have amended the phrase to recite -dot- before the word “gov” instead of a period. Applicants respectfully assert that this would not be construed as an active web link once published on the USPTO web site. Withdrawal of the objection is respectfully requested.

***The Rejection of Claim 1 Under 35 U.S.C. § 112 First Paragraph***

Claim 1 stands rejected under 35 U.S.C. § 112 first paragraph for allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the art that the inventors had possession of the claimed invention at the time of filing. The Office Action asserts that claim 1 “does not provide support for all variations of the gene that lie outside the fragment.”

Applicants point out that claim 1 does not read on “variations of the gene that lie outside of the fragment” as asserted in the Office Action. Claim 1 uses “closed” claim language with the recitation of the phrase “consisting of” to modify the claimed contiguous bases selected from the Markush group of SEQ ID NOS. Accordingly, the claimed sequences cannot be interpreted to include variations that lie outside of the fragment consisting of at least about 100 contiguous bases of a sequence selected from the group consisting of SEQ ID NOS:2, 3, 4, 5, 6, 8, 9 and 10. Applicants respectfully assert that the claimed sequences are fully disclosed in the application as-filed and that the inventors were in possession of the claimed invention as of the filing date. Withdrawal of the rejection is requested.

***The Rejection of Claims 11-15 Under 35 U.S.C. § 102(b)***

Claims 11-15 stand rejected under 35 U.S.C. § 102(b) as allegedly being anticipated by De Beenhouwer *et al.* (WO 95/33851).

The Office Action alleges that the ‘851 publication anticipates the claims because “De Beenhouwer *et al.*’s probe is a contiguous probe of 319 bp length contains [sic] a portion which is

perfectly complementary to bp 41-63 of SEQ ID NO:7...” Applicants respectfully disagree with the grounds of the rejection for the following reasons:

The claims are drawn to polynucleotide probes or primers that hybridize under stringent hybridization conditions to specific sequences identified in the claims by SEQ ID NO. without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO:1. The claims further require that said stringent hybridization conditions comprise 5 x SSPE and a temperature of 25-30 °C.

Nothing in the cited De Beenhouwer reference teaches or suggests the claimed probes or primers because the sequences disclosed in De Beenhouwer would not hybridize to the recited SEQ ID NOS under the required hybridization conditions. The Office Action identifies a 22 bp probe and a 319 bp probe, both of which are alleged to be perfectly complementary to a portion of SEQ ID NO:7 (Office Action at page 6). Applicants respectfully point out that SEQ ID NO:7 is not recited in any of claims 11-15. Accordingly, these disclosures have no bearing on the claims.

Finally, the Office Action alleges that De Beenhouwer teaches a sequence of 324 bp contiguous length which contains 72 contiguous base pairs that are complementary to SEQ ID NO:10 (Office Action at page 5). The Office Action also alleges that De Beenhouwer teaches a 319 nucleotide sequence that contains a stretch of 67 contiguous base pairs that are 100% complementary to SEQ ID NO:8. Applicants respectfully point out that SEQ ID NO:8 and SEQ ID NO:10 are both 705 bases in length. Under the required stringent hybridization conditions, Applicants respectfully assert that the disclosed DNA fragments of 324 and 319 nucleotides would not hybridize to the recited sequences. Accordingly, these disclosures have no bearing on the claims. Withdrawal of the rejection is requested.

***New Grounds of Rejection Necessitated by the Amendment of January 6, 2003  
The Rejection of Claims 11-16 under 35 U.S.C. § 112, First Paragraph***

Claims 11-16 stand rejected under 35 U.S.C. § 112 first paragraph for allegedly containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the art that the inventors had possession of the claimed invention at the time of filing.

The Office Action alleges that Applicants have not indicated where in the specification support for limitations “ ‘at least about 5’ bases that differ from SEQ ID NO:1” may be found.

Without acquiescing to the grounds of the rejection, Applicants have amended claims 11-16 such that this phrase is no longer recited. Withdrawal of the rejection is requested.

***The Rejection of Claim 1 Under 35 U.S.C. § 112 Second Paragraph***

Claim 1 stands rejected under 35 U.S.C. § 112 second paragraph for allegedly being indefinite for its recitation of “consisting of at least about.” The Office Action alleges that combining the term “consisting of” with the term “at least about” contravenes the established meaning of “consisting of” by reopening the closed claim language.

Applicants respectfully traverse the rejection for the following reasons. Claim 1 uses “closed” claim language because it uses the phrase “consisting of” to modify the claimed contiguous bases selected from the Markush group of SEQ ID NOS. The term “at least about” modifies the lower limit of the size of the claimed sequences and does not “reopen the closed language” as is asserted in the Office Action because it only modifies the lower limit of the size of the claimed sequences. Accordingly, Applicants respectfully assert that there is no indefiniteness in claim 1. Withdrawal of the rejection is requested.

***Indication of Allowable Subject Matter***

Applicants acknowledge, with appreciation, the indication at page 8 of the Office Action that claims 2-10 are allowable.

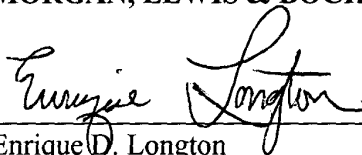
***Conclusion***

In view of the foregoing remarks, Applicants respectfully request withdrawal of all outstanding rejections and early notice of allowance to that effect. Should the Examiner believe that a telephonic interview would expedite prosecution and allowance of this application, he is encouraged to contact the undersigned at his convenience.

Except for issue fees payable under 37 C.F.R. § 1.18, the Commissioner is hereby authorized by this paper to charge any additional fees during the entire pendency of this application including fees due under 37 C.F.R. §§ 1.16 and 1.17 which may be required, including any required extension of time fees, or credit any overpayment to Deposit Account No.50-0310. This paragraph is intended to be a **CONSTRUCTIVE PETITION FOR EXTENSION OF TIME** in accordance with 37 C.F.R. § 1.136(a)(3).

Respectfully submitted,

**MORGAN, LEWIS & BOCKIUS LLP**



Enrique D. Longton  
Reg. No. 47,304

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**Customer No. 000033522**  
**MORGAN, LEWIS & BOCKIUS LLP**  
1111 Pennsylvania Ave., N.W.  
Washington, DC 20004  
202.739.3000 (voice)  
202.739.3001 (fax)